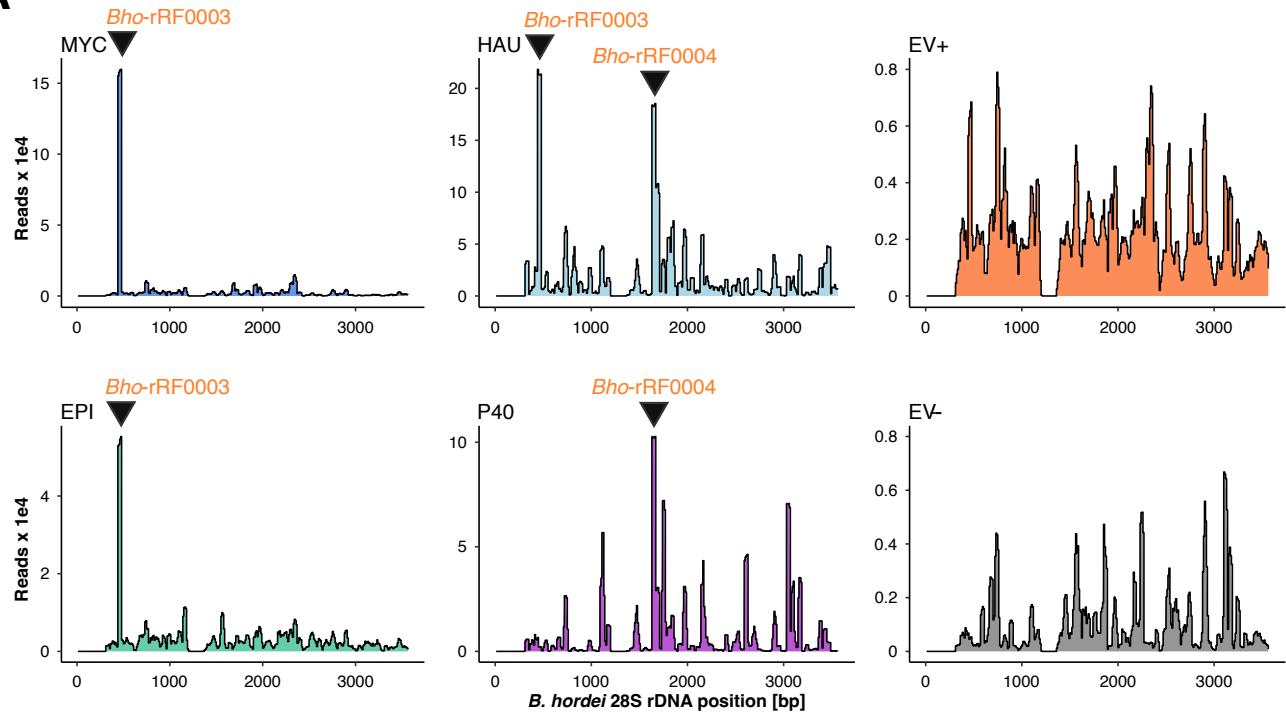
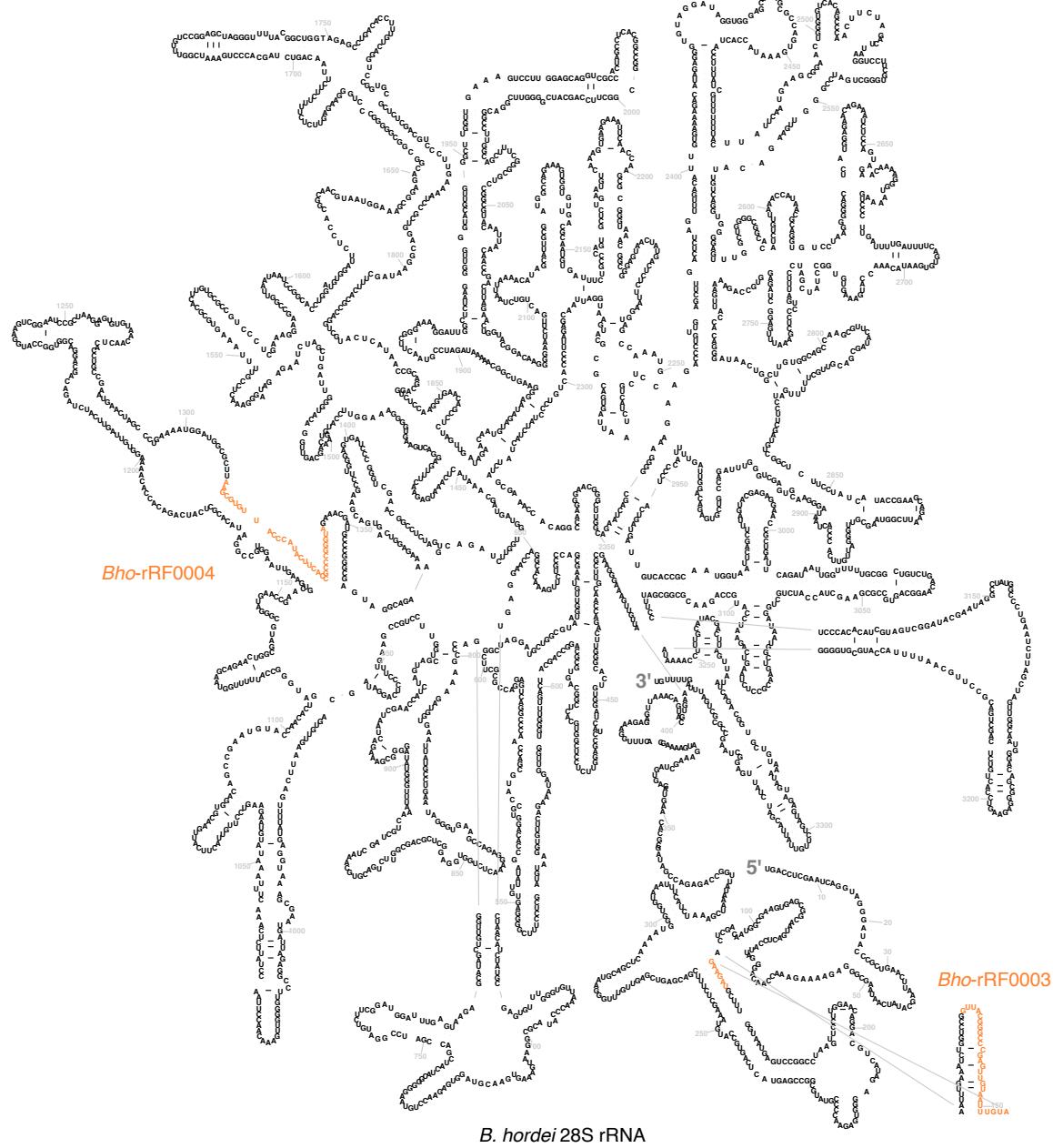


A**B**

Supplementary Figure 5. Specific *B. hordei* 28S rRNA-derived sRNAs are enriched in the 31-33 bases long reads. (A) We aligned sRNA sequencing reads of 31-33 bases to the *B. hordei* 28S rDNA (3,564 bases). The graphs display the number of reads identified (y-axis) mapping to each position of the *B. hordei* 28S rDNA (x-axis). Epiphytic fungal mycelium (MYC), infected epidermis without mycelium (EPI), fungal haustoria (HAU), microsomes of the epidermis without haustoria (P40), apoplastic extracellular vesicles (EV+), and apoplastic extracellular vesicles of non-infected control plants (EV-). (B) Secondary structure of the 28S rRNA of *B. hordei* (RFAM accessions CAUH01009223.1:1667-1 and CAUH01013050.1:1126-1; RNA central accession URS0000C6B9A3_546991; full structure was reconstructed from these partial fragments) predicted by R2DT in RNA central (<https://rnacentral.org>). The RNA stretches shown in orange indicate the over-represented 28S rRNA fragments *Bho-rRF0003* and *Bho-rRF0004* from the Myc, Epi, Hau, and P40 samples.